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OM protein - protein search, using sw model

Run on: December 25, 2004, 12:29:37 ; Search time 73 seconds

(without alignments)
535.637 Million cell updates/sec

Title: US-10-063-728-114

Perfect score: 595
Sequence: 1 MWMVLVLLLPFLTKSVFCSL.....ABPLSGCGFGGPGCGRRRD 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_238sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	595	100.0	109	3	AAy94964 Human sec
2	595	100.0	109	3	AAy87344 Human sig
3	595	100.0	109	3	AAy94424 Human PRO
4	595	100.0	109	4	AAy66173 Protein o
5	595	100.0	109	4	AAU29195 Human PRO
6	595	100.0	109	4	AAy87582 Human PRO
7	595	100.0	109	5	ABG95907 Human sec
8	595	100.0	109	5	ABUS8571 Human PRO
9	595	100.0	109	6	ABUS8119 Novel hum
10	595	100.0	109	6	ABUS8434 Human sec
11	595	100.0	109	6	ABR6308 Human sec
12	595	100.0	109	6	ABR6569 Human sec
13	595	100.0	109	6	ABUS9638 Human sec
14	595	100.0	109	6	ABUS2877 Human PRO
15	595	100.0	109	6	ABUS9998 Human sec
16	595	100.0	109	6	ABR68247 Human sec
17	595	100.0	109	6	ABUS6300 Novel hum
18	595	100.0	109	6	ABUS92731 Human sec
19	595	100.0	109	6	ABO08808 Human sec
20	595	100.0	109	6	ABO02860 Human sec
21	595	100.0	109	6	ABR75014 Human sec
22	595	100.0	109	6	ABR94776 Human sec
23	595	100.0	109	6	ABUS5749 Human PRO
24	595	100.0	109	6	ABUS9909 Novel hum
25	595	100.0	109	6	ABUS8124 Novel hum

26	595	100.0	109	6	ABUS1830 Novel hum
27	595	100.0	109	6	ABUS9523 Human PRO
28	595	100.0	109	6	ABUS6364 Human sec
29	595	100.0	109	6	ABUS7577 Human sec
30	595	100.0	109	6	ABUS0605 Human PRO
31	595	100.0	109	6	ABUS9032 Novel hum
32	595	100.0	109	6	ABO33991 Human sec
33	595	100.0	109	6	ABR99523 Human sec
34	595	100.0	109	6	ABR98913 Human sec
35	595	100.0	109	6	ABO16436 Human sec
36	595	100.0	109	6	ABR92336 Human sec
37	595	100.0	109	6	ABO18977 Human sec
38	595	100.0	109	6	ABR78398 Human sec
39	595	100.0	109	6	ABUS72008 Novel hum
40	595	100.0	109	6	ABUS5134 Novel hum
41	595	100.0	109	6	ABO00273 Novel hum
42	595	100.0	109	6	ABO11605 Human sec
43	595	100.0	109	6	ABO02250 Human sec
44	595	100.0	109	6	ABUS8824 Novel hum
45	595	100.0	109	6	ABUS3519 Human sec

ALIGNMENTS

RESULT 1	AAy94964	Human secreted protein clone QY442.2 protein sequence SEQ ID NO:134.
ID	AAy94964	standard; protein, 109 AA.
XX		
AC	AAy94964;	
XX		
DT	16-JUN-2000	(first entry)
XX		
DE	Human secreted protein clone QY442.2 protein sequence SEQ ID NO:134.	
XX		
KW	Human; secreted protein; immunostimulant; immunosuppressant; virucide;	
KW	antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;	
KW	antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide;	
KW	antihiroid; immune deficiency; severe combined immunodeficiency; SCID;	
KW	infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;	
KW	connective tissue disease; multiple sclerosis; erythematosis;	
KW	rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;	
KW	Gullain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;	
KW	insulin dependent diabetes mellitus; graft-versus-host disease;	
KW	autoimmune inflammatory eye disease; allergy.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200009552-A1.	
XX		
PD	24-FEB-2000.	
XX		
PF	13-AUG-1999;	99WO-US018298.
XX		
PR	14-AUG-1998;	98US-0096622P.
PR	17-AUG-1998;	98US-0096615P.
PR	04-SEP-1998;	98US-0099229P.
PR	23-OCT-1998;	98US-0105368P.
PR	08-JAN-1999;	99US-0115234P.
PR	12-FEB-1999;	99US-0119931P.
PR	18-FEB-1999;	99US-0120575P.
PR	30-APR-1999;	99US-0132020P.
PR	11-AUG-1999;	99US-0148424P.
XX		
PA	(GENY) GENETICS INST INC.	
XX		
PI	Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;	
PI	Wenberg D, Treacy M, Agostino MJ, Steinger RJ, Spaulding V;	
PI	Wong GG, Clark HF, Pechtel K;	
XX		
DR	WPI; 2000-205979/18.	
XX		
PT	New polynucleotides encoding secreted proteins, which may have e.g.	

PT nutritional, chemokine, immune stimulating or suppressing, hematopoiesis
PT regulating, tissue growth, activin/inhibin antiinflammatory or tumor
PT inhibition activity.
PS Claim 143, Page 595, 61pp, English.
XX
CC AAA16618 to AAA16697 encode the human secreted proteins given in AAY94898
CC to AAY94880, isolated from human adult brain, adult thyroid, adult
CC retina, foetal carcinoma, adult blood, adult neural, foetal kidney, adult
CC placenta, adult testis, whole embryo, adult cartilage, kidney, foetal
CC brain, adult thymus, foetal placenta, adult uterus, adult tumour, and
CC adult bladder, cDNA libraries. The polynucleotides and proteins are
CC predicted to have biological activities which would make them suitable
CC for treating, preventing or ameliorating medical conditions in humans and
CC animals. The polynucleotides can be used as markers for tissues in which
CC the protein is preferentially expressed, as molecular weight markers on
CC Southern gels, and as chromosome markers or tags to identify chromosomes
CC or to map gene positions. The proteins can be used in the treatment of
CC immune deficiencies and disorders, such as severe combined
CC immunodeficiency (SCID), as well as viral, bacterial, fungal and other
CC infections. These infections include human immunodeficiency virus (HIV),
CC hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and
CC candidiasis. The proteins can be used to treat autoimmune disorders such
CC as connective tissue disease, multiple sclerosis, systemic lupus
CC erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation,
CC Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent
CC diabetes mellitus, myasthenia gravis, graft-versus-host disease and
CC autoimmune inflammatory eye disease. The proteins can also be used to
CC treat allergic conditions, such as asthma. AAA16698 to AAA16774 represent
CC probes for the human secreted proteins from the present invention
XX
SQ Sequence 109 AA;
* Query Match 100.0%; Score 595; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 2e-55;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 M L M W V L L L P T L K S V F C S L V T S L Y L P N T E D L S L M L M P K D L H S G R T E V S T H T V P S K G 60
Db 1 M L M W V L L L P T L K S V F C S L V T S L Y L P N T E D L S L M L M P K D L H S G R T E V S T H T V P S K G 60
Qy 61 T A S P C W P L A G A V P S P T V S R L E A L T R A V Q V A E P L G S C G F G C P G C R R R D 109
Db 61 T A S P C W P L A G A V P S P T V S R L E A L T R A V Q V A E P L G S C G F G C P G C R R R D 109
RESULT 2
AAY87344
ID AAY87344 standard; protein, 109 AA.
XX
AC AAY87344;
XX
XX 11-MAY-2000 (first entry)
XX
XX Human signal peptide containing protein HSP-121 SEQ ID NO:121.
XX
XX Human signal peptide-containing protein; HSP; diagnosis; cancer;
XX inflammation; cardiovascular disease; anticancer; anti-inflammatory;
XX antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
XX antiasthmatic; gene therapy; cell proliferation; neurological disorder;
XX reproductive disorder; developmental disorder; arteriosclerosis;
XX cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
XX asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
XX Parkinson's disease; Huntington's disease; ovulatory defect;
XX muscular dystrophy.
XX
XX Homo sapiens.
XX
XX WO200000610-A2.
XX
XX 06-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US014484.
XX
XX PF

XX
XX 26-JUN-1998; 98US-0090762P.
XX 31-JUL-1998; 98US-0094983P.
XX 01-OCT-1998; 98US-0102686P.
XX 11-DEC-1998; 98US-0112129P.
XX
XX (INCYTE PHARM INC.
XX
XX Lal P, Tang YT, Gorsone GA, Corley NC, Guegler KJ, Baughn MR,
XX Akerblom IE, Au-Yang J, Yue H, Patterson C, Reddy R, Hillman JL,
XX Bandman O;
XX
XX WPI; 2000-160673/14.
XX N-PDB; AA298229.
XX
XX New human signal peptide-containing proteins useful in treatment,
XX prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
XX disease.
XX
XX Claim 1, Page 240, 327pp, English.
XX
XX AAA298109 to AA298242 encode AAY87224 to AAY87357 which represent the
XX human signal peptide-containing proteins HSP-1 to HSP-134. HSPPs have
XX anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
XX neuroprotective, cardiovascular and antiasthmatic activities, and can be
XX used in gene therapy. HSPPs can be used to treat or prevent disorders
XX associated with decreased activity or function of HSP. Antagonists of
XX HSP are used to treat or prevent disorders associated with increased
XX activity or function of HSP. Such diseases include cell proliferation
XX (including cancer), inflammation, cardiovascular, neurological,
XX reproductive or developmental disorders, (e.g. arteriosclerosis,
XX cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
XX asthma, Crohn's disease, microbial or other infections, congestive or
XX ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
XX diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
XX nucleic acids can be used for the recombinant production of HSP, for
XX detecting HSP in standard hybridisation and amplification assays (for
XX diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
XX or ribozyme therapeutics, for detecting related sequences or genetic
XX variations, and for chromosomal mapping. HSP are also used to raise
XX specific antibodies (Ab) and to screen for agonists and antagonists
XX (potential therapeutic agents). Ab are used to diagnose, or monitor, HSP
XX -related diseases (in usual immunoassays), as therapeutic antagonists, in
XX competitive drug screens, and for purification of HSP from natural
XX sources
XX
SQ Sequence 109 AA;
* Query Match 100.0%; Score 595; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 2e-55;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 M L M W V L L L P T L K S V F C S L V T S L Y L P N T E D L S L M L M P K D L H S G R T E V S T H T V P S K G 60
Db 1 M L M W V L L L P T L K S V F C S L V T S L Y L P N T E D L S L M L M P K D L H S G R T E V S T H T V P S K G 60
Qy 61 T A S P C W P L A G A V P S P T V S R L E A L T R A V Q V A E P L G S C G F G C P G C R R R D 109
Db 61 T A S P C W P L A G A V P S P T V S R L E A L T R A V Q V A E P L G S C G F G C P G C R R R D 109
RESULT 3
AAY99424
ID AAY99424 standard; protein, 109 AA.
XX
XX AAY99424;
XX
XX 08-AUG-2000 (first entry)
XX
XX Human PRO1446 (UNQ740) amino acid sequence SEQ ID NO:304.
XX
XX Human PRO polypeptide; membrane bound protein; receptor; diagnosis;
XX transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
XX KW

XX	Hom sapiens.	98US-0098716P
XX		98US-0098749P
XX		98US-0098750P
PN	MO200012708-A2.	98US-0098803P
XX		98US-0098821P
XX		98US-0098843P
XX		98US-0099536P
XX		98US-0099596P
XX		98US-0099588P
XX		98US-0099602P
XX		98US-0099642P
XX		98US-0099741P
XX		98US-0099754P
XX		98US-0099763P
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XX		98

PR	06-OCT-1998;	98US-0103449P.
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PR	07-OCT-1998;	98US-0103315P.
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PR	07-OCT-1998;	98US-0103401P.
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PR	08-OCT-1998;	98US-0103678P.
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PR	20-OCT-1998;	98US-0105000P.
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PR	20-OCT-1998;	98US-0105002P.
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PR	21-OCT-1998;	98US-0105104P.
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PR	22-OCT-1998;	98US-0105169P.
XX		
PR	22-OCT-1998;	98US-0105266P.
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PR	26-OCT-1998;	98US-0105693P.
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PR	27-OCT-1998;	98US-0105810P.
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PR	27-OCT-1998;	98US-0105882P.
XX		
PR	27-OCT-1998;	98US-0106062P.
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PR	28-OCT-1998;	98US-0106029P.
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PR	28-OCT-1998;	98US-0106032P.
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PR	28-OCT-1998;	98US-0106033P.
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PR	28-OCT-1998;	98US-0106178P.
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PR	29-OCT-1998;	98US-0106248P.
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PR	29-OCT-1998;	98US-0106384P.
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PR	29-OCT-1998;	98US-0106387P.
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PR	30-OCT-1998;	98US-0106464P.
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PR	03-NOV-1998;	98US-0106856P.
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PR	03-NOV-1998;	98US-0106902P.
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PR	03-NOV-1998;	98US-0106905P.
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PR	03-NOV-1998;	98US-0106912P.
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PR	03-NOV-1998;	98US-0106932P.
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PR	03-NOV-1998;	98US-0106934P.
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PR	10-NOV-1998;	98US-0107783P.
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PR	17-NOV-1998;	98US-0108775P.
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PR	17-NOV-1998;	98US-0108779P.
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PR	17-NOV-1998;	98US-0108787P.
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PR	17-NOV-1998;	98US-0108802P.
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PR	18-NOV-1998;	98US-0108858P.
XX		
PR	18-NOV-1998;	98US-0108904P.
XX		
EA	(GETH) GENENTECH INC.	
XX		
PI	Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;	
XX		
DR	WPI; 2000-237871/20.	
XX		
DR	N-PDB; AAA37106.	
XX		
PT	New mammalian DNA sequences encoding transmembrane, receptor or secreted	
XX	Pro polypeptides, useful for screening of potential peptide or small	
PT	molecule inhibitors of the relevant receptor/ligand interactions.	
XX		
XS	Claim 12; Fig 170; 773bp; English.	
XX		
CC	AAA37022 to AAA37144 encode the new isolated human transmembrane,	

CC receptor or secreted PRO polypeptides given in AAY9340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC transmembrane peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding them have various industrial applications and nucleotide sequences
CC pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent PCR
CC primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention
XX
XX Sequence 109 AA;

Query Match 100.0%; Score 595; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 2e-55;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLMWLVLLLPPTKSVFCSIVTSLYLPNTEDLSLWMPKPDLSGTRTEVSTHTVPSKPG 60
DB 1 MLMWLVLLLPPTKSVFCSIVTSLYLPNTEDLSLWMPKPDLSGTRTEVSTHTVPSKPG 60

QY 61 TASPQWPLAGAVPSPTVSRLEALTRAVQVAEPVSGSGFGGPGCGRRRD 109
DB 61 TASPQWPLAGAVPSPTVSRLEALTRAVQVAEPVSGSGFGGPGCGRRRD 109

RESULT 4
AAB6173
ID AAB6173 standard; protein; 109 AA.
XX
XX AAB6173;
XX
XX 02-APR-2001 (first entry)
XX
XX Protein of the invention #85.
XX
XX Secreted; transmembrane; gene therapy.
XX
XX Unidentified.
XX
XX WO200078961-A1.
XX
XX 28-DEC-2000.
XX
XX 18-FEB-2000; 2000WO-US004342.
XX
XX 23-JUN-1999; 99US-0141037P.
XX
XX 20-JUL-1999; 99US-0144758P.
XX
XX 26-JUL-1999; 99US-0145698P.
XX
XX 01-SEP-1999; 99WO-US020111.
XX
XX 29-OCT-1999; 99US-0162506P.
XX
XX 30-NOV-1999; 99WO-US028313.
XX
XX 02-DEC-1999; 99WO-US028551.
XX
XX 16-DEC-1999; 99WO-US030095.
XX
XX 05-JAN-2000; 2000WO-US000219.
XX
XX 06-JAN-2000; 2000WO-US000376.
XX
XX
XX (GENTECH) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX
XX Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX
XX Williams PM, Wood WI;
XX
XX WPI; 2001-071395/08.
XX
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
XX
XX PT useful as hybridization probes, in chromosome and gene mapping and gene
XX
XX therapy.
XX
XX Claim 1; Fig 170; 787pp; English.
XX
XX The present invention relates to secreted and transmembrane proteins.
XX
XX CC These proteins and the DNA encoding them may be used as hybridization
XX
XX probes, in chromosome and gene mapping and in the generation of anti-

CC sense RNA and DNA. They may also be used used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
XX
XX acids may also be used in gene therapy
XX
XX Sequence 109 AA;

Query Match 100.0%; Score 595; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 2e-55;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLMWLVLLLPPTKSVFCSIVTSLYLPNTEDLSLWMPKPDLSGTRTEVSTHTVPSKPG 60
DB 1 MLMWLVLLLPPTKSVFCSIVTSLYLPNTEDLSLWMPKPDLSGTRTEVSTHTVPSKPG 60

QY 61 TASPQWPLAGAVPSPTVSRLEALTRAVQVAEPVSGSGFGGPGCGRRRD 109
DB 61 TASPQWPLAGAVPSPTVSRLEALTRAVQVAEPVSGSGFGGPGCGRRRD 109

RESULT 5
AAU29195
ID AAU29195 standard; protein; 109 AA.
XX
XX AAU29195;
XX
XX 18-DEC-2001 (first entry)
XX
XX
XX Human PRO polypeptide sequence #172.
XX
XX
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
XX
XX dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
XX
XX blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
XX
XX adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
XX Homo sapiens.
XX
XX
XX WO200168848-A2.
XX
XX 20-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US006520.
XX
XX 01-MAR-2000; 2000WO-US005601.
XX
XX 02-MAR-2000; 2000WO-US005841.
XX
XX 03-MAR-2000; 2000US-0187202P.
XX
XX 05-MAR-2000; 2000US-0186568P.
XX
XX 14-MAR-2000; 2000US-0189320P.
XX
XX 15-MAR-2000; 2000US-0189328P.
XX
XX 21-MAR-2000; 2000WO-US006884.
XX
XX 21-MAR-2000; 2000US-0190828P.
XX
XX 21-MAR-2000; 2000US-0191007P.
XX
XX 21-MAR-2000; 2000US-0191048P.
XX
XX 21-MAR-2000; 2000US-0191314P.
XX
XX 28-MAR-2000; 2000US-0192655P.
XX
XX 29-MAR-2000; 2000US-0193032P.
XX
XX 29-MAR-2000; 2000US-0193053P.
XX
XX 30-MAR-2000; 2000WO-US008439.
XX
XX 04-APR-2000; 2000US-0194449P.
XX
XX 04-APR-2000; 2000US-0194647P.
XX
XX 11-APR-2000; 2000US-0195975P.
XX
XX 11-APR-2000; 2000US-0196000P.
XX
XX 11-APR-2000; 2000US-0196187P.
XX
XX 11-APR-2000; 2000US-0196690P.
XX
XX 11-APR-2000; 2000US-0196820P.
XX
XX 18-APR-2000; 2000US-0198121P.
XX
XX 18-APR-2000; 2000US-0198585P.
XX
XX 25-APR-2000; 2000US-0199397P.
XX
XX 25-APR-2000; 2000US-0199550P.
XX
XX 25-APR-2000; 2000US-0199654P.
XX
XX 17-MAY-2000; 2000US-0201516P.
XX
XX 17-MAY-2000; 2000WO-US013705.
XX
XX 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 20-DEC-2000; 2000MO-US034956.

XX (GETH) GENENTECH INC.

PA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX MPI; 2001-602746/68.

DR N-PSDB; AAS46096.

XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.

XX Claim 11; Fig 344; 774pp; English.

XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumor in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumor in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumor necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumors and also
 CC susceptibility to tumor development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumors, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX SQ

Sequence 109 AA;

Query Match 100.0%; Score 595; DB 4; Length 109;
 .. Best Local Similarity 100.0%; Pred. No. 2e-55; 0; Indels 0; Gaps 0;
 Matches 109; Conservative 0; Mismatches 0;

QY 1 MWMVLVLLPTLKSVFCSLVLTSLYPTNEDLSLWMPKPDLSGRTREVSHTVPSKPG 60
 DB 1 MWMVLVLLPTLKSVFCSLVLTSLYPTNEDLSLWMPKPDLSGRTREVSHTVPSKPG 60
 QY 61 TASPCCWPLAGAVPSPVSRLEALTRAQVAEPLGSCGFGCPGRRRD 109
 DB 61 TASPCCWPLAGAVPSPVSRLEALTRAQVAEPLGSCGFGCPGRRRD 109

RESULT 6

AB87582
 ID AAB87582 standard; protein; 109 AA.

XX AAB87582;

XX 15-MAY-2001 (first entry)

DE Human PRO1446.

XX Human; PRO protein; mapping.

XX Homo sapiens.

XX WO200116318-A2.

XX 08-MAR-2001.

XX 24-AUG-2000; 2000MO-US023328.

XX 01-SEP-1999; 99MO-US020111.

PR 15-SEP-1999; 99MO-US021090.

PR 07-DEC-1999; 99US-0169495P.

PR 09-DEC-1999; 99US-0170262P.

PR 11-JAN-2000; 2000US-0175481P.

PR 18-FEB-2000; 2000MO-US004342.

PR 22-FEB-2000; 2000MO-US004414.

PR 01-MAR-2000; 2000MO-US005601.

PR 03-MAR-2000; 2000US-0187202P.

PR 21-MAR-2000; 2000US-0191007P.

PR 30-MAR-2000; 2000MO-US008439.

PR 25-APR-2000; 2000US-0199397P.

PR 22-MAY-2000; 2000MO-US014042.

PR 05-JUN-2000; 2000US-0209832P.

XX (GETH) GENENTECH INC.

PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CU, Gurney AL, Watanabe CK, Wood WI;
 XX MPI; 2001-183260/18.

DR N-PSDB; AAF92114.

XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
 PT biology, including use as hybridization probes, and in chromosome and
 PT gene mapping.

XX Claim 12; Fig 114; 278pp; English.

XX The present sequence is a human PRO polypeptide (secreted and
 CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
 CC anti-PRO antibodies are useful for preparation of a medicament useful in
 CC the treatment of a condition which is responsive to the PRO protein,
 CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
 CC employed as molecular weight markers for protein electrophoresis. The PRO
 CC coding sequence has applications in molecular biology, including use as
 CC hybridization probes, and in chromosome and gene mapping
 XX SQ

Sequence 109 AA;

Query Match 100.0%; Score 595; DB 4; Length 109;
 .. Best Local Similarity 100.0%; Pred. No. 2e-55; 0; Indels 0; Gaps 0;
 Matches 109; Conservative 0; Mismatches 0;

QY 1 MWMVLVLLPTLKSVFCSLVLTSLYPTNEDLSLWMPKPDLSGRTREVSHTVPSKPG 60
 DB 1 MWMVLVLLPTLKSVFCSLVLTSLYPTNEDLSLWMPKPDLSGRTREVSHTVPSKPG 60
 QY 61 TASPCCWPLAGAVPSPVSRLEALTRAQVAEPLGSCGFGCPGRRRD 109
 DB 61 TASPCCWPLAGAVPSPVSRLEALTRAQVAEPLGSCGFGCPGRRRD 109

RESULT 7

ABG5907
 ID ABG5907 standard; protein; 109 AA.

XX ABG5907;

XX 10-DEC-2002 (first entry)

DE Human secreted/transmembrane protein PRO1446.

XX Human; secreted protein; transmembrane protein; antirheumatic;
 KW antiarthritis; osteoarthritis; sports-related joint problem;
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.

XX Homo sapiens.

XX 08-MAR-2001.

PN US2002119130-A1.
 XX 29-AUG-2002.
 XX 06-DEC-2001; 2001US-00006867.
 XX 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 22-APR-1998; 98US-0082797P.
 PR 22-APR-1998; 98US-0083495P.
 PR 15-MAY-1998; 98US-0085579P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088740P.
 PR 10-JUN-1998; 98US-0088811P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088825P.
 PR 11-JUN-1998; 98US-0088863P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 19-JUN-1998; 98US-0089952P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 24-JUN-1998; 98US-0090444P.
 PR 25-JUN-1998; 98US-0090688P.
 PR 25-JUN-1998; 98US-0090686P.
 PR 26-JUN-1998; 98US-0090862P.
 PR 02-JUL-1998; 98US-0091628P.
 PR 10-AUG-1998; 98US-0096012P.
 PR 17-AUG-1998; 98US-0096757P.
 PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 26-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 08-MAR-1999; 99US-00505028.
 PR 14-MAY-1999; 99US-00510733.
 PR 02-JUN-1999; 99US-00520111.
 PR 01-SEP-1999; 99US-00520111.
 PR 15-SEP-1999; 99US-00521194.
 PR 22-DEC-1999; 99US-00530720.
 PR 18-FEB-2000; 2000US-00504342.
 PR 18-FEB-2000; 2000US-00504342.
 PR 22-FEB-2000; 2000US-00504414.
 PR 01-MAR-2000; 2000US-00505601.
 PR 30-MAR-2000; 2000US-00508439.
 PR 22-MAY-2000; 2000US-00514042.
 PR 02-JUN-2000; 2000US-00515264.
 PR 23-AUG-2000; 2000US-00523522.
 PR 24-AUG-2000; 2000US-00523528.

PR 10-NOV-2000; 2000US-005030873.
 PR 01-DEC-2000; 2000US-00523378.
 PR 20-DEC-2000; 2000US-00534956.
 PR 28-FEB-2001; 2001US-0006520.
 PR 01-MAR-2001; 2001US-0006666.
 PR 30-MAY-2001; 2001US-0017443.
 PR 01-JUN-2001; 2001US-0017800.
 PR 20-JUN-2001; 2001US-0019692.
 PR 29-JUN-2001; 2001US-0021066.
 PR 09-JUL-2001; 2001US-0021735.

(GENTH) GENENTECH INC.

PI Easton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX WPI; 2002-721348/79.
 DR N-PSDB; ABS74434.

PT New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.

XX Claim 20; Fig 114; 399pp; English.

XX The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as
 CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing an A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1899 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for
 CC identifying agonists or antagonists, for the preparation of a medicament
 CC useful in the treatment of a condition which is responsive to the
 CC proteins, as molecular weight markers for protein electrophoresis
 CC purposes, and as therapeutic agents for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid
 CC arthritis. Nucleic acids encoding the proteins are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to
 CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic useful reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence represents a novel secreted or transmembrane protein of the
 CC invention

XX Sequence 109 AA;

Query Match 100.0%; Score 595; DB 5; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2e-55; 0; Indels 0; Gaps 0;
 Matches 109; Conservative 0; Mismatches

QY 1 MWMVLLVLLPTLKSVCFLVSTLYLPTNEDLSLIMLMPKDLHSGRTVEVSTHTVPSKRG 60
Db 1 MWMVLLVLLPTLKSVCFLVSTLYLPTNEDLSLIMLMPKDLHSGRTVEVSTHTVPSKRG 60
QY 61 TASPCCPLAGAVPSPTVSRLEALTRAVOVAEPIGSCGPGGPGGRRD 109
61 TASPCCPLAGAVPSPTVSRLEALTRAVOVAEPIGSCGPGGPGGRRD 109
Db 61 TASPCCPLAGAVPSPTVSRLEALTRAVOVAEPIGSCGPGGPGGRRD 109
RESULT 8
ABUS8571
ID ABUS8571 standard; protein; 109 AA.
XX
AC ABUS8571;
XX
DT 15-APR-2003 (first entry)
XX
DE Human PRO polypeptide #172.
XX
KW Human; PRO; cytosolic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADERT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027272-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176492.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
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PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
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BR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
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PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
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PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
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PR 22-APR-1998; 98US-0082797P.
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PR 05-MAY-1998; 98US-0084366P.
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PR 07-MAY-1998; 98US-0084639P.
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PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
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PR 02-JUN-1998; 98US-0087609P.
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PR 26-JUN-1998; 98US-0090862P.
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PR 01-JUL-1998; 98US-0091359P.
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PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.

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PR 02-JUL-1998; 98US-0091626P.
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PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
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Query Match 100.0%; Score 595; DB 6; Length 109;
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XX
DT 07-JUL-2003 (first entry)
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DE Novel human secreted and transmembrane protein PRO1446.
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KW Human, secreted and transmembrane protein; PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
PN US2003032127-A1.
XX
PD 13-FEB-2003.
XX
PF 26-JUN-2002; 2002US-00183012.
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Db 61 TASPCWPLAGAVSPPTVSRLEALTRAVQVAEPLGSCGFQGGPCGRRD 109
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XX
AC ABUS4434;
XX
DT 02-AUG-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) #172.
XX
KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KM tissue typing.
XX
OS Homo sapiens.
PN US2003032112-A1.
XX
PD 13-FEB-2003.
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PF 21-JUN-2002; 2002US-00176756.
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RESULT 11
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ID ABR66308 standard; protein; 109 AA.
XX
AC ABR66308;
XX
DT 05-AUG-2003 (first entry)
XX
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XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritis; vulnery; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003027278-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176987.
XX
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XX 05-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO1446, SEQ ID NO:344.
XX
XX Human; PRO; secreted protein; transmembrane protein;
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX Chondrocyte; proliferation; differentiation; cartilage disorder;
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX adrenal tumour; lung; colon; breast; prostate; kidney; cervix;
XX liver; drug screening; transgenic animal; genetic analysis;
XX antiarthritic; vulnereary; gene therapy.
XX
OS Homo sapiens.
XX
XX US2003036159-A1.
XX
PD 20-FEB-2003.
XX
XX
PF 02-JUL-2002; 2002US-00188773.
XX
XX 18-SEP-1997; 97US-0059263P.
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PR 10-SEP-1998; 98US-0099741P.
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Query Match 100.0%; Score 595; DB 6; Length 109;
Best Local Similarity 100.0%; Pred. No. 2e-55;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MWMVLLVLLPTKSVFCSTVTSYLPTNTEDLSIMLMPKPDLSGCTEYVSTHTVPSKPG 60
QY 61 TASPCCWLAGAVPSPTVSRLEALTRAVQVAEPLGSCFGGCPGRRRD 109
DB 61 TASPCCWLAGAVPSPTVSRLEALTRAVQVAEPLGSCFGGCPGRRRD 109

RESULT 13
ABU99638
ID ABU99638 standard; protein; 109 AA.
XX
AC ABU99638;
XX

DT 09-AUG-2003 (First entry)
DE
XX Human secreted/transmembrane protein (PRO) #172.
XX
XX Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
OS Homo sapiens.
XX
PN US2003040070-A1.
PD
XX 27-FEB-2003.
XX
PF 27-JUN-2002; 2002US-00184627.
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PR 07-OCT-1998; 98US-0016897P;

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Best Local Similarity 100.0%; Pred. No. 2e-55;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MMTMTVLLPTLKSYFGSLVTSIYIPNTEDISLMTWPKDLSGRTIVSTHTVPSKGG 60
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DB 61 TASPCEPLAGAVPSPTVSRLEALTRAVOVAEPPLGSGFGGCPGRRRD 109

RESULT 14
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XX ABU82877;
AC ABU82877;
XX 27-JUN-2003 (first entry)
DT 27-JUN-2003 (first entry)
XX Human PRO polypeptide #172.
DE

XX Human; PRO polypeptide; secreted and transmembrane protein; tumour;
KW Chromosome mapping; gene mapping; cytostatic.
XX Homo sapiens.
OS US2003032113-A1.
XX 13-FEB-2003.
PD 20-JUN-2002; 2002US-00176911.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
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PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
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Query Match 100.0%; Score 595; DB 6; Length 109;
Best Local Similarity 100.0%; Pred. No. 28-55;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 TASPCCPLAGAVPSPTVSRLEALTRAVQVAEPIGSCGCGPCGRRRD 109

RESULT 15

ABU89998
ID ABU89998 standard; protein; 109 AA.

XX AC ABU89998;

XX DT 11-AUG-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO1446.

XX KM Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;

KW Chondrocyte differentiation; tumour necrosis factor-alpha release;

KW affinity purification.
XX Homo sapiens.
OS $\frac{1}{3}$
XX US2003036147-A1.
XX 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00187741.
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Query Match 100.0%; Score 595; DB 6; Length 109;
Best Local Similarity 100.0%; Pred. No. 2e-55; Indels 0; Gaps 0;
Matches 109; Conservative 0; Mismatches 0;

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D b 61 T A S P C W P L A G A V P S P T V S R I E A L T R A V O A E P I G S C G F O G G P C G R R D 109

Search completed: December 25, 2004, 16:31:07
Job time : 75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 14:35:27 ; Search time 22 Seconds
(without alignments)
476.710 Million cell updates/sec

Title: US-10-063-728-114

Perfect score: 595

Sequence: 1 MLMWLVLLPTLKSVFCSL.....AEPLGSCGPGGCPGRRRD 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR 79:*
2: p1r1:*
3: p1r2:*
4: p1r3:*
5: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	80.5	13.5	217	2 S01358	salivary glue prot
3	79.5	13.4	1102	2 JH0717	guanylate cyclase
4	75.5	12.7	393	1 S06594	cellular tumor ant
5	74.5	12.5	555	2 T04146	glyoxyl homolog -
6	73.5	12.4	627	2 D75193	serine proteinase,
7	73	12.3	224	2 C48652	transfer protein s
8	73	12.3	841	2 AG2250	nitrogen assimilat
9	72	12.1	391	2 JC6193	tumor suppressor p
10	71.5	12.0	335	2 T44498	hypothetical prote
11	71.5	12.0	340	1 WMBE11	latency-related pr
12	71.5	12.0	450	2 B82957	probable aminotran
13	71	11.9	845	2 T12537	hypothetical prote
14	70.5	11.8	274	2 T20435	hypothetical prote
15	70.5	11.8	464	2 S75831	hypothetical prote
16	70.5	11.8	553	2 A49364	59 protein, brain
17	70	11.8	440	2 S52895	TYA protein - yeas
18	70	11.8	501	2 C49830	hypothetical prote
19	70	11.8	835	2 S75842	nitrogen assimilat
20	69.5	11.7	503	2 H70509	hypothetical prote
21	69.5	11.7	2055	2 T00093	hypothetical prote
22	69	11.6	120	2 F72643	hypothetical prote
23	69	11.6	259	2 S76205	hypothetical prote
24	69	11.6	522	2 S52316	hypothetical prote
25	68.5	11.5	359	2 B56731	chromatin assembl
26	68.5	11.5	4859	2 S74173	ryanodine receptor
27	68	11.4	1751	2 A45604	major blood-stage
28	67.5	11.3	236	2 F64964	yeap protein - Esc
29	67.5	11.3	453	1 S49013	transforming prote

30	67.5	11.3	615	2 T34392	hypothetical prote
31	67.5	11.3	662	1 UYPVNA	noncapsid protein
32	67.5	11.3	872	2 S33015	hypothetical prote
33	67.5	11.3	992	2 A31666	hypothetical prote
34	67.5	11.3	1215	2 S50428	probable Ca2+-tran
35	67	11.3	130	2 G72609	hypothetical prote
36	67	11.3	441	2 A43555	GAP-43-related pro
37	67	11.3	475	2 G83028	N-acetylmutramoyl-L
38	67	11.3	2629	2 T10987	telomerase-associat
39	66.5	11.2	118	2 S54309	hypothetical 13.2K
40	66.5	11.2	684	2 A53019	collagen alpha 1(X
41	66.5	11.2	982	2 T19171	hypothetical prote
42	66.5	11.2	3566	1 A40701	tenascin-X precurs
43	66	11.1	187	2 T50610	hypothetical prote
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45	66	11.1	302	2 T40490	probable 26s prote

ALIGNMENTS

RESULT 1
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probable ABC transporter, ATP-binding protein Sma2079 [imported] - Sinorhizobium meliloti
C/Species: Sinorhizobium meliloti
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C/Accession: G95403
R/Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kaiman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yen, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A/Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A/Reference number: A95262; MUID:21396509; PMID:11481432
A/Accession: G95403
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-314 <KUR>
A/Cross-references: UNIPROT:Q92XV5; GB:AE006469; PDB:AAK65793.1; PID:g14524294; GSPDB:G
R/Salber, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federici, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
A/Authors: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
Science 293, 668-672, 2001
A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A/Reference number: A96039; MUID:21368234; PMID:11474104
A/Contents: annotation
A/Genetics:
A/Genes: Sma2079
A/Genome: plasmid
C/Superfamily: inner membrane protein malK; ATP-binding cassette homology
Query Match 14.1%; Score 84; DB 2; Length 314;
Best local Similarity 30.7%; Pred. No. 0.95;
Matches 27; Conservative 14; Mismatches 29; Indels 18; Gaps 4;
QY 17 FCSLVTSYLTV---PTEPLSLWLPKPDHSGSTRTEVSTHVPKSGTASCMPLAGAV 72
DB 213 FCDRLVWYLGKRVASADDETMSDP--HPTRALMAAVDPSPRQAA---PLGSEL 266
QY 73 PSPT-----VSRLEALTRAVOVAEP 92
DB 267 PPSNPFGCRPHTRCPALTELCRAVEP 294
RESULT 2
S01358
salivary glue protein sgs-3 precursor - fruit fly (Drosophila simulans)
C/Species: Drosophila simulans
C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C/Accession: S01358; A29388
R/Martin, C.H.; Mayeda, C.A.; Meyerowitz, E.M.
J. Mol. Biol. 201, 273-287, 1988

QY 9 LPLTKSVFCSGLVTSYLPTNTEDLSLMLKPKDLHSGRTREVSHTVPSKPGTASPCWPL 68
DB 88 LARTLADAFWGPGLTLLPLPSAQV-----PDVAVTGKATVGIR-VPDGPVALALIERF 139
QY 69 AGAVPSPTVSRLLEAL--TRAVQVAPPLG---SCFGGPGPC 103
DB 140 GGGTAAPSANRFGKRVSTTAHVAADLCGRVDVLVDGPGC 179

RESULT 11
MBE11
latency-related protein 1 - human herpesvirus 1 (strain F)
C:Species: human herpesvirus 1
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A33337
R:Mechanism: S.L.; Neaburn, A.B.; Zwaagstra, J.; Ghiasi, H.
Virology 168, 168-172, 1989
A:Title: Sequence of the latency-related gene of herpes simplex virus type 1.
A:Reference number: A94388; PMID:89085598; PMID:2535901
A:Accession: A33337
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-340 <MEC>
A:Cross-references: UNIPROT:P17588; GB:J04323; NID:G330133; PIDN:AAA45799.1; PID:G330134
C:Genetics:
A:Introns: 249/2
C:Superfamily: herpesvirus latency-related protein 1
C:Keywords: tandem repeat
F:26-41/Region: 16-residue tandem repeat
F:42-57/Region: 16-residue tandem repeat
E:58-73/Region: 16-residue tandem repeat

Query Match 12.0%; Score 71.5; DB 1; Length 340;
Best Local Similarity 37.1%; Pred. No. 17;
Matches 23; Conservative 5; Mismatches 29; Indels 5; Gaps 3;

QY 33 SLMLMPKPDLSGRTREVSHTT-VPSKPGTASPCWPLAGVPSPTVSRLLEALTRAVQVAP 91
DB 14 ALMLTPEPAQH-GRTPTPHSHAPPLRPTTPSHPSHRAPLD--RAPTPHSHAP 69

QY 92 PL 93
DB 70 PL 71

RESULT 12
B82957
Probable aminotransferase PA5523 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: B82957
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.T.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
A:Reference number: A82950; PMID:20437337; PMID:10984043
A:Accession: B82957
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-450 <STO>
A:Cross-references: UNIPROT:Q9HT50; GB:AE004964; GB:AE004091; NID:G9951849; PIDN:AG0890
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5523

Query Match 12.0%; Score 71.5; DB 2; Length 450;
Best Local Similarity 26.6%; Pred. No. 23;
Matches 21; Conservative 9; Mismatches 28; Indels 21; Gaps 3;

QY 38 PKPDLHS-----GRTREV-STHTVPSKPGTASPCW-----PLAGVPSPT 76

DB 221 PQGFHQKRLRLRRHGTLLIDETHITSTGGCGTBAWKLEPPDTLCKPIAGVPCSV 280
QY 77 VSRLEALTRAVQVAPPLG 95
DB 281 YGCSAAMASAMQIARARAS 299

RESULT 13
T12537
hypothetical protein DKFZp434H244.1 - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12537
R:Mambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17524
A:Accession: T12537
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-313;314-845 <MAN>
A:Cross-references: UNIPROT:O14841; EMBL:AL096750
A:Experimental source: adult testis; clone DKFZp434H244
A:Note: the cDNA sequence contains a -1 frameshift near codon 313
C:Genetics:
A:Note: DKFZp434H244.1
C:Superfamily: hypothetical protein YKL215C

Query Match 11.9%; Score 71; DB 2; Length 845;
Best Local Similarity 33.3%; Pred. No. 51;
Matches 24; Conservative 6; Mismatches 38; Indels 4; Gaps 2;

QY 33 SLMLMPKPDLSGRTREVSHTTVPSPKPGTASPCWPLAGVPSPTVSRLLEALTRAVQVAP 92
DB 42 SLMLGFSQ--QERTQDPATATKRVIRIWPWCPLAAGPAPVSPITAAVSCSPASSP 99

QY 93 LG--SCFGGPG 102
DB 100 QAPHPVHLPGP 111

RESULT 14
T20435
hypothetical protein E03G2.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20435
R:McMurry, A.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19275
A:Accession: T20435
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-274 <WIL>
A:Cross-references: UNIPROT:Q27276; EMBL:Z68113; PIDN:CAA92149.1; GSPDB:GN00028; CESP:E03
A:Experimental source: clone E03G2
C:Genetics:
A:Gene: CESP:E03G2.3
A:Map position: X
A:Introns: 42/3; 89/2; 197/3; 239/3

Query Match 11.8%; Score 70.5; DB 2; Length 274;
Best Local Similarity 26.8%; Pred. No. 17;
Matches 34; Conservative 17; Mismatches 43; Indels 33; Gaps 6;

QY 5 LVLLPLTKSVFCSGLVTSYL-----PNTEDLSLMLKPKDLHSGRTREVSHTVPS 57
DB 3 LVLLPLTSSITCYCALDTAAVAIAIQTEINKSHADIEML-----DHVKINARVSDIGRPG 58

QY 58 KPQT-ASPCWP-----LAGAVPSPTVSRLLEAL--TRAVQV-APPLG 95
DB 59 PGTNGSPGPGSKGRKGRSDGKCSVAGVSLDKKEKVEITLEFDLSNETPVLRLAN 118

QY	96	CGFQGGP	102
Db	119	PGSTGQP	125

RESULT 15

S75831
hypothetical protein glr1285 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
V:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S75831
R:Kaneko, T., Sato, S., Kotani, H., Tanaka, A., Asamizu, E., Nakamura, Y., Miyajima, N.,
O. K., Okumura, S., Shimpo, S., Takeuchi, C., Wada, T., Watanabe, A., Yamada, M., Yasuda,
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
S.
A:Reference number: S74332; MUID:97061201; PMID:8905231
A:Accession: S75831
A:Status: nucleic acid sequence not shown, translation not shown
A:Molecule type: DNA
A:Residues: 1-464 <KAN>
A:Cross-references: UNIPROT:P74139, EMBL:D90913, GB:AB001339, NID:g1653348, PTDN:BA018230
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
C:Start codon: GTG

Query Match	11.8%	Score	70.5	DB	2	Length	466
Best Local Similarity	31.1%	Pred.	No. 30				
Matches	28	Conservative	8	Mismatches	45	Indels	9
						Gaps	2

QY 13 LKSFCSLVTSLVLPTEPELST-----WLPKPKDLSGRTREVSHTVPSKKGTSAPC 65

Db 159 LQQAAMSLQARKLTKGSLSPDLSLLQKTTIAAFNFPQDFFDLVTVFPQGLMDVQPNVYNIIPC 218

QY 66 WPLAGAVPSPPTYSRLTALTRAVQVAEPPLGS 95

Db 219 QEQESAPSPDVELLQALTH--EVRPIPLTS 246

Search completed: December 25, 2004, 16:31:36
Job time : 24 secs

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1	595	100.0	109	2	06W64	06W64 homo sapien
2	593	100.0	109	2	AAQ89316	AAQ89316 homo sapien
3	93	15.6	414	2	06VIL8	06VIL8 streptomyc
4	93	15.6	414	2	AAQ84166	AAQ84166 streptomyc
5	92	15.5	381	1	P53 CANA	029537 canis fami
6	84.5	14.2	385	2	095376	095376 canis fami
7	84.5	14.2	386	1	P53 BELCA	P41685 felis b
8	84	14.1	314	2	092XV5	092XV5 thizobium n
9	80.5	13.5	217	1	SGS3_DROSI	P13729 dirosophila
10	80.5	13.5	269	1	HXA9_MORSA	09W45 morone saxea
11	79.5	13.4	690	2	08PE02	08PE02 xanthomonaa
12	77.5	13.0	536	2	093Q78	093Q78 rhodococcu
13	77	12.9	554	2	09P8U3	09P8U3 aspergillus
14	76.5	12.8	401	2	08XSC3	08XSC3 raietonia e
15	76	12.8	369	2	08NCU7	08NCU7 homo sapien
16	75.5	12.7	267	2	09PV07	09PV07 oryzae lat
17	75.5	12.7	393	1	P53_CERAE	P13481 cericophilhec
18	75.5	12.7	769	2	09KR24	09KR24 streptococc
19	75.5	12.7	769	2	09KK40	09KK40 streptococc
20	75.5	12.7	769	2	09FDD1	09FDD1 streptococc
21	75.5	12.7	2284	2	09VP81	09VP81 drosophila
22	75	12.6	329	2	08ZNI5	08ZNI5 salmonella
23	75	12.6	351	2	08XWPI	08XWPI raietonia e
24	74.5	12.5	555	5	004693	004693 oryza sativa
25	74	12.4	387	2	08SP23	08SP23 delphinapet
26	74	12.4	493	3	07W4S1	07W4S1 bordetella
27	74	12.4	493	2	07MG97	07MG97 bordetella
28	74	12.4	644	2	08BKX2	08BKX2 mus musculu
29	73.5	12.4	515	2	06P227	06P227 xenopus t
30	73.5	12.4	515	2	AAH64237	AAH64237 xenopus t
31	73.5	12.4	627	2	09RUD0	09RUD0 deinococcu

32	Q85WT7	2	665	12.4	73.5	32	O85WT7	O85WT7	drosophila
33	Q8PQX0	2	710	12.4	73.5	33	Q8PQX0	Q8PQX0	xanthomona
34	Q9VTK2	2	886	12.4	73.5	34	Q9VTK2	Q9VTK2	drosophila
35	Q8LS84	2	1213	12.4	73.5	35	Q8LS84	Q8LS84	oryza sativa
36	Q07193	2	224	12.3	73	36	Q07193	007193	streptomyces
37	Q8YR90	2	841	12.3	73	37	Q8YR90	Q8YR90	anabaena sp
38	Q6Z0G5	2	431	12.2	72.5	38	Q6Z0G5	Q6Z0G5	oryza sativa
39	BAD03641	2	431	12.2	72.5	39	BAD03641	BAD03641	oryza sativa
40	BAD12953	1	431	12.2	72.5	40	BAD12953	BAD12953	oryza sativa
41	P53.RABIT	1	331	12.1	72	41	P53.RABIT	Q95330	oryctolagus
42	Q6DFY6	1	835	12.1	72	42	Q6DFY6	Q6DFY6	mus musculus
43	FLXB.HUMAN	1	1162	12.1	72	43	FLXB.HUMAN	Q9Y2K7	homo sapiens
44	AA64360	1	1162	12.1	72	44	AA64360	AA64360	homo sapiens
45	Q6SL40	2	217	12.0	71.5	45	Q6SL40	Q6SL40	amillifer

ALIGNMENTS

Query Match	Best Local Similarity	Score	DB 2	Length	109
Matches	109	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0
QY	1	MLMWLVLLPTLTKSVFCSLVTSLYLPNTEDLSLWLPKPDHSGTRTVSHTHVPKRG	60		
DB	1	MLMWLVLLPTLTKSVFCSLVTSLYLPNTEDLSLWLPKPDHSGTRTVSHTHVPKRG	60		
QY	61	TASPCWPLAGVPSPTVSRLEALRAVOVAPPLSCGCGGPGPCGRPD	109		
DB	61	TASPCWPLAGVPSPTVSRLEALRAVOVAPPLSCGCGGPGPCGRPD	109		
RESULT 2					
ID	AAQ89316	PRELIMINARY;	PRT;	109 AA.	
AC	AAQ89316;				
DT	02-MAR-2004	(TREMBLrel. 27, Created)			
DT	02-MAR-2004	(TREMBLrel. 27, Last sequence update)			
DT	02-MAR-2004	(TREMBLrel. 27, Last annotation update)			
GN	PINK1.				
OS	ORFNames=UNQ740;				
OC	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo;				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=22887296; PubMed=12975309;				
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,				
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,				
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,				
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,				
RA	Lewis L., Lito D., Mark W., Robbie E., Sanchez C., Schoenfeld J.,				
RA	Sehagiri S., Simmons L., Singh V., Smith V., Stinson J., Vagts A.,				
RA	Vanclen R., Watanabe C., Wiand D., Woods K., Xie M.H., Yanura D.,				
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,				
RA	Godowski P.;				
RT	"The secreted protein discovery initiative (SPDI), a large-scale				
RT	effort to identify novel human secreted and transmembrane proteins: a				
RT	bioinformatics assessment."				
RL	Genome Res. 13:2265-2270(2003).				
DR	EMBL; AY358957; AAQ89316.1; --				
SO	SEQUENCE 109 AA; 11822 MW; ABA6C475792E2B73 CRC64;				

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,
RA Eaton D., Foster J., Gilmaldi C., Gu Q., Hase P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagstad A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL, AY358957; AA089316.1; -.
SQ SEQUENCE 109 AA; 11822 MW; ABA6C475792E2B73 CRC64;

Query Match 100.0%; Score 595; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.9e-47;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWMVLLLPFTKSVCSLVTSYLPTNTEDLSLWMPKPDHSGTREVSTHVPKPG 60
DB 1 MWMVLLLPFTKSVCSLVTSYLPTNTEDLSLWMPKPDHSGTREVSTHVPKPG 60

QY 61 TASCWPLAGAVPSPVSRLEALTRAVQVAEPLGSCGFGGCPGRRRD 109
DB 61 TASCWPLAGAVPSPVSRLEALTRAVQVAEPLGSCGFGGCPGRRRD 109

RESULT 3
Q6VLI8 PRELIMINARY; PRT; 414 AA.
AC Q6VLI8;
DT 05-JUL-2004 (TRENDELrel. 27, Created)
DT 05-JUL-2004 (TRENDELrel. 27, Last sequence update)
DE 05-JUL-2004 (TRENDELrel. 27, Last annotation update)
DE P1MS4.
GN Name=P1MS4;
OS Streptomyces sp. HK803;
OC Bacteria; Actinobacteria; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=244967;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=HK803;
RC MEDLINE=22841069; PubMed=12819191;
RA Palanlappan N., Kim B.S., Sekiyama Y., Osada H., Reynolds K.A.;
RT "Enhancement and selective production of phosphatase B, a protein
RT phosphatase Iia inhibitor, through identification and engineering of
RT the corresponding biosynthetic gene cluster.";
RL J. Biol. Chem. 278:35552-35557(2003).
DR EMBL, AY354515; AA084166.1; -.
DR PROSITE, PS50850; MFS; 1.
DR PROSITE, PS50850; MFS; 1.
SQ SEQUENCE 414 AA; 42040 MW; 90604A1085F6C6F5 CRC64;
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Query Match 15.6%; Score 93; DB 2; Length 414;
Best Local Similarity 29.9%; Pred. No. 2.3;
Matches 35; Conservative 12; Mismatches 42; Indels 28; Gaps 5;
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QY 3 MWMVLLLPFTKSVCSLVTSYLPTNTEDLSLWMPKPDHSGTREVSTHVPKPG 53
DB 108 WMPVVVVV-----ALVTGLSAVPVSGISRAVWPKIVGSELSTLYTAATASVITTT 159
QY 54 TVPSKP-----GTASPCWPLAGAVPSPVSRLEALTRAVQVAEPLGSCGFGGCPGRR 106
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```
DB 160 TGPLLASLVIAVAGPYWAVG-----VTALLALVSALVFMAALGRAGVGGEPLPQR 209

RESULT 4
AA084166 PRELIMINARY; PRT; 414 AA.
AC AA084166;
DT 02-MAR-2004 (TRENDELrel. 27, Created)
DT 02-MAR-2004 (TRENDELrel. 27, Last sequence update)
DE 02-MAR-2004 (TRENDELrel. 27, Last annotation update)
DE P1MS4.
GN P1MS4.
OS Streptomyces sp. HK803;
OC Bacteria; Actinobacteria; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=244967;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=HK803;
RC MEDLINE=22841069; PubMed=12819191;
RA Palanlappan N., Kim B.S., Sekiyama Y., Osada H., Reynolds K.A.;
RT "Enhancement and Selective Production of Phosphatase B, a Protein
RT Phosphatase Iia Inhibitor, through Identification and Engineering of
RT the Corresponding Biosynthetic Gene Cluster.";
RL J. Biol. Chem. 278:35552-35557(2003).
DR EMBL, AY354515; AA084166.1; -.
SQ SEQUENCE 414 AA; 42040 MW; 90604A1085F6C6F5 CRC64;
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Query Match 15.6%; Score 93; DB 2; Length 414;
Best Local Similarity 29.9%; Pred. No. 2.3;
Matches 35; Conservative 12; Mismatches 42; Indels 28; Gaps 5;
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```
QY 3 MWMVLLLPFTKSVCSLVTSYLPTNTEDLSLWMPKPDHSGTREVSTHVPKPG 53
DB 108 WMPVVVVV-----ALVTGLSAVPVSGISRAVWPKIVGSELSTLYTAATASVITTT 159
QY 54 TVPSKP-----GTASPCWPLAGAVPSPVSRLEALTRAVQVAEPLGSCGFGGCPGRR 106
DB 160 TGPLLASLVIAVAGPYWAVG-----VTALLALVSALVFMAALGRAGVGGEPLPQR 209
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```
RESULT 5
P53 CANFA STANDARD; PRT; 381 AA.
AC 029537; Q9TV78;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN Name=TP53; Synonyms=P53;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Leukocyte;
RC MEDLINE=98178696; PubMed=9519881;
RA Veldhoen N., Milner J.;
RT "Isolation of canine p53 cDNA and detailed characterization of the
RT full length canine p53 protein.";
RL Oncogene 16:1077-1084(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Spleen;
RA Setoguchi A., Sekai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
RA Watarai T., Hasagawa A., Tsujimoto H.;
RT "Aberrations of p53 tumor suppressor gene in various spontaneous
RT tumors in the dog.";
RN [3]
RP SEQUENCE OF 25-300 FROM N.A.
RX STRAIN=Beagle;
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RX MEDLINE=95323915; PubMed=7600529;
 RA Kraegel S.A., Pazzi K.A., Madewell B.R.;
 RT "Sequence analysis of canine p53 in the region of exons 3-8.";
 RL Cancer Lett. 92:181-186(1995).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -1- PTM: Phosphorylated on Thr-18 by VRK1, which may prevent the
 CC interaction with MDM2 (By similarity).
 CC -1- PTM: Acetylated. Its deacetylation by SIRT1 impairs its ability to
 CC induce proapoptotic program and modulate cell senescence (By
 CC similarity).
 CC -1- DISEASE: P53 is found in increased amounts in a wide variety of
 CC transformed cells. P53 is frequently mutated or inactivated in
 CC many types of cancer.
 CC -1- SIMILARITY: Belongs to the p53 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF060514; AAC16909.1; -;
 CC EMBL; AB020761; BAA78379.1; -;
 CC EMBL; S77819; AAB42022.1; -;
 CC HSSP; P04637; 1GZH.
 CC InterPro: IPR002117; P53.
 CC InterPro: IPR008967; P53_like_DNA_bnd.
 CC InterPro: IPR010991; P53_tetramerictn.
 CC Pfam; PF00870; P53; 1.
 CC PRINTS; PR00386; P53SUPPRESSR.
 CC ProDom; PD002681; P53; 1.
 CC PROSITE; PS00348; P53; 1.
 CC Acetylation; Activator; Anti-oncogene; Apoptosis; DNA-binding;
 CC Metal-binding; Nuclear protein; Phosphorylation;
 CC Transcription regulation; Zinc.
 CC FT DOMAIN 1 44 Transcription activation (acidic).
 CC FT DOMAIN 89 280 By similarity.
 CC FT DOMAIN 313 344 Oligomerization.
 CC FT DOMAIN 327 338 Nuclear export signal (By similarity).
 CC FT DOMAIN 356 375 BASIC (REPRESSION OF DNA-BINDING).
 CC FT DOMAIN 293 309 Bipartite nuclear localization signal (By
 CC similarity).
 CC FT METAL 163 163 Zinc (By similarity).
 CC FT METAL 166 166 Zinc (By similarity).
 CC FT METAL 226 226 Zinc (By similarity).
 CC FT METAL 230 230 Zinc (By similarity).
 CC FT MOD_RES 15 15 Phosphoserine (By PPPK) (By similarity).
 CC FT MOD_RES 18 18 Phosphothreonine (by VRK1) (By
 CC similarity).
 CC FT MOD_RES 361 361 N6-acetyllysine (By similarity).
 CC FT MOD_RES 370 370 N6-acetyllysine (By similarity).
 CC FT BINDING 380 380 RNA (covalent) (By similarity).
 CC FT CONFLICT 1 4 MERS -> MQGP (in Ref. 2).
 CC FT CONFLICT 378 378 L -> P (in Ref. 2).
 CC SEQUENCE 381 AA; 42486 MW; 761A718PDC3DA59 CRC64;
 Query Match 15.5%; Score 92; DB 1; Length 381;
 Best Local Similarity 38.6%; Pred. No. 2.6;
 Matches 27; Conservative 6; Mismatches 27; Indels 10; Gaps 4;

QY 9 LLP---TLKSVCSLVTSVLTPTNEDLSLWMPKPDLSGRTVSTHTVPSKPGTASRC 65
 Db 25 LIPENNVLSSELCPAVDELLLP--ESVNVWL-----DESDDAPRMPATSAPTAPGPA--PS 77
 QY 66 WPLAGAVPSP 75
 Db 78 WPLSSVSPSP 87
 RESULT 6
 ID 095326 PRELIMINARY; PRT; 285 AA.
 AC 095326;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE P53 protein (Fragment).
 GN Name=P53;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_Taxid=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang B.-J., Shi X.B., Lau D.H.M.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -1- SIMILARITY: Belongs to the p53 family.
 CC EMBL; U62133; AAB16961.1; -;
 CC HSSP; P04637; 1GZH.
 CC GO; GO:0005634; C:nucleus; IEA.
 CC GO; GO:0003700; P:transcription factor activity; IEA.
 CC GO; GO:0006915; P:apoptosis; IEA.
 CC GO; GO:0045786; P:negative regulation of cell cycle; IEA.
 CC GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
 CC InterPro: IPR002117; P53.
 CC InterPro: IPR008967; P53_like_DNA_bnd.
 CC Pfam; PF00870; P53; 1.
 CC PRINTS; PR00386; P53SUPPRESSR.
 CC ProDom; PD002681; P53; 1.
 CC PROSITE; PS00348; P53; 1.
 CC Activator; Anti-oncogene; Apoptosis; Cell cycle; DNA-binding;
 CC Metal-binding; Nuclear protein; Phosphorylation;
 CC Transcription regulation; Zinc.
 CC FT NON_TER 1 1
 FT NON_TER 285 285
 SQ SEQUENCE 285 AA; 31616 MW; 673427DBBF8BCECE CRC64;
 Query Match 14.2%; Score 84.5; DB 2; Length 285;
 Best Local Similarity 37.7%; Pred. No. 9.4;
 Matches 23; Conservative 6; Mismatches 25; Indels 7; Gaps 3;
 QY 15 SYFCSVTSVLTPTNEDLSLWMPKPDLSGRTVSTHTVPSKPGTASPCWPLAGAVPS 74
 Db 2 SELCPAVDELLLP--ESVNVWL-----DESDDAPRMPATSAPTAPGPA--PSWPLSSVPS 54
 QY 75 P 75
 Db 55 P 55
 RESULT 7

P53_FELCA
ID P53_FELCA STANDARD; PRT; 366 AA.
AC P41685;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN Name=TP53; Synonyms=TRP53;
OS Fels silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RX MEDLINE=94333960; PubMed=8056458;
RA Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Yoon H.Y.,
RA Watarai T., Goitsuka R., Tsujimoto H., Hasegawa A.;
RT "Cloning of feline p53 tumor-suppressor gene and its aberration in
hematopoietic tumors."
RL Int. J. Cancer 58:602-607(1994).
RN [2]
RP SEQUENCE OF 34-354 FROM N.A.
RX MEDLINE=94114693; PubMed=8286534;
RA Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watarai T., Goitsuka R.,
RA O'Brien S.J., Tsujimoto H., Hasegawa A.;
RT "Molecular cloning and chromosomal mapping of feline p53 tumor
suppressor gene."
RL J. Vet. Med. Sci. 55:801-805(1993).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
BAX and FAS antigen expression, or by repression of Bcl-2
expression.
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -1- PFM: Phosphorylated on Thr-18 by VRK1, which may prevent the
interaction with MDM2 (By similarity).
CC -1- PFM: Acetylated. Its deacetylation by SIRT1 impairs its ability to
induce proapoptotic program and modulate cell senescence (By
similarity).
CC -1- DISBASE: p53 is found in increased amounts in a wide variety of
transformed cells. p53 is frequently mutated or inactivated in
many types of cancer.
CC -1- SIMILARITY: Belongs to the p53 family.
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CC -----
DR EMBL; D26608; BAA05653.1; -;
DR EMBL; D16460; BAA03927.1; -;
DR HSSP; P04637; 1GZH.
DR InterPro; IPR002117; p53.
DR InterPro; IPR008967; p53_like_DNA_bnd.
DR InterPro; IPR010991; p53_tetrameriscn.
DR Pfam; PF00870; p53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; p53; 1.
DR PROSITE; PS00348; p53; 1.
DR Acetylation; Acivator; Anti-oncogene; Apoptosis; DNA-binding;
KW Metal-binding; Nuclear protein; Phosphorylation;
KW Transcription regulation; Zinc.
FT DOMAIN 1 44 Transcription activation (acidic).

FT DNA_BIND 94 285
FT DOMAIN 318 349 By similarity.
FT DOMAIN 332 343 Oligomerization.
FT DOMAIN 361 380 Nuclear export signal (By similarity).
FT DOMAIN 298 314 BASIC (REPRESSION OF DNA-BINDING).
FT METAL 168 168 Bipartite nuclear localization signal (By
similarity).
FT METAL 171 171 Zinc (By similarity).
FT METAL 231 231 Zinc (By similarity).
FT METAL 235 235 Zinc (By similarity).
FT MOD_RES 15 15 Phosphoserine (by PPPK) (By similarity).
FT MOD_RES 18 18 Phosphothreonine (by VRK1) (By
similarity).
FT MOD_RES 366 366 N6-acetyllysine (By similarity).
FT MOD_RES 375 375 N6-acetyllysine (By similarity).
FT BINDING 385 385 RNA (covalent) (By similarity).
FT CONFLICT 285 285 K -> R (in Ref. 2).
SQ SEQUENCE 386 AA; 42692 MW; D08B43BA1BC8EB78 CRC64;
Query Match 14.2%; Score 84.5; DB 1; Length 386;
Best local similarity 37.5%; Pred. No. 13;
Matches 27; Conservative 10; Mismatches 24; Indels 11; Gaps 4;
QY 9 LPTKSVPCSLVTSLY--LPNTEDSLWMPRDDHSGRTREVSHTVPSKRGTSPC- 65
Db 25 LTRP-NNVLSSSELSANNELPLSEEDVANWLDPAIPDASG---MSAVPAPAPAPATPAP 79
QY 66 ---WPLAGAVPS 74
Db 80 AISMPLSSFPVS 91
RESULT 8
Q92XV5 PRELIMINARY; PRT; 314 AA.
ID Q92XV5
AC Q92XV5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable ABC transporter, ATP-binding protein.
GN OrderedLocustNames=RA1135; ORFNames=SWA2079;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymA.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barloy-Hubler F., Bowser L., Capela D., Gallibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kaiman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federapfel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti pSymA megaplasmid."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21368234; PubMed=11474104;
RA Gallibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
RA Boutry M., Bowser L., Bunimaster U., Cadieu E., Capela D., Chain P.,
RA Cowie A., Davis R.W., Dreano S., Federapfel N.A., Fisher R.F.,
RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA Kahn M.L., Kaiman S., Keating D.H., Kies E., Komp C., Lelaure V.,
RA Masny D., Palm C., Peck M.C., Pohl T.M., Portetle D., Punnelle B.,
RA Ramseberger U., Surzycki R., Thebaud P., Vandewol M.,
RA Vorholter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
RT "The composite genome of the legume symbiont Sinorhizobium meliloti."


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Q8PE02
ID Q8PE02 PRELIMINARY; PRT; 690 AA.
AC Q8PE02;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein KCC0181.
GN OrderedLocustNames=XCC0181;
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=340;
RX [1]
SEQUENCE FROM N.A.
RP STRAIN=ATCC 33913 / NCPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Canavan F., Cardozo J., Chabergo F., Clapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madela A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Midanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sana J.A.D., Silva C., de Souza R.F.,
RA Spinoja L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Teza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White E.F.,
RA Seubal J.C., Kltajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL: AE012114; AAA39500.1; -.
DR InterPro: IPR001440; TPR.
DR InterPro: IPR008941; TPR-like.
DR Pfam: PF00515; TPR; 6.
DR SMART: SM00028; TPR; 5.
DR PROSITE: PS50005; TPR; 1.
DR PROSITE: PS50293; TPR_REGION; 1.
KM Complete proteome; Hypothetical protein; Repeat; TPR repeat.
SQ SEQUENCE 690 AA; 75528 MW; 733A01F0DEBAC3 CRC64;

Query Match 13.4%; Score 79.5; DB 2; Length 690;
Best Local Similarity 28.6%; Pred. No. 70;
Matches 28; Conservative 8; Mismatches 39; Indels 23; Gaps 4;

QY 19 SLVTSLYPNTEDISLMLW-----PKPDHSGT---RFEVSTHTVPSKPGTASPC--W 66
DB 395 SLIESLPAPQQTIVLRPWIGNVQDRAGQPDALATWQFHEHQDHRPLRPQAKFPMQW 454
QY 67 PLGAVP-----SPTVSRLELTLRAVQVAEFL 93
DB 455 PPGVSTPDTVSARPLFWGPPGSHVERLIAVMDATPL 492

RESULT 12
Q93078
ID Q93078 PRELIMINARY; PRT; 536 AA.
AC Q93078;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Benzotetra dioxigenase reductase.
GN Name=dogZ;
OS Rhodococcus sp. 19070.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
NCBI_TaxID=161384;
RX [1]
SEQUENCE FROM N.A.
RP STRAIN=19070;

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RX MEDLINE=21268842; PubMed=11715157;
RA Haddad S., Eby D.M., Neidle E.L.;
RT "Cloning and expression of the benzotetra dioxigenase genes from
RT Rhodococcus sp. strain 19070."
RL Appl. Environ. Microbiol. 67:2507-2514(2001).
DR EMBL: AF279141; AAK58905.1; -.
DR HSP; P07771; ICRH.
DR GO: GO:0005489; F:electron transporter activity; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0016702; F:oxidoreductase activity; acting on single d. .; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR006058; 2Fe2S_id_BS.
DR InterPro: IPR008990; E_transp_acc.
DR InterPro: IPR008333; FAD_binding_6.
DR InterPro: IPR001041; Ferredoxin.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR InterPro: IPR001221; Phe_hydroxylase.
DR Pfam: PF00970; FAD_binding_6; 1.
DR Pfam: PF00111; Fer2; 1.
DR PRINTS: PR00175; NAD_binding_1; 1.
DR PRINTS: PR00371; FENCR.
DR PRINTS: PR00410; PHEHYDRIASE.
DR PROSITE: PS00197; 2FE2S_FERREDOXIN; 1.
KM 2Fe-2S; Dioxigenase; Iron; Iron-sulfur.
SQ SEQUENCE 536 AA; 58643 MW; 97ED577853B5982D CRC64;

Query Match 13.0%; Score 77.5; DB 2; Length 536;
Best Local Similarity 25.7%; Pred. No. 82;
Matches 27; Conservative 10; Mismatches 35; Indels 33; Gaps 4;

QY 10 LPTIKSVFC-----SLVTSLYLP---NTEDLSLMLWPKPDHSGTREVSTHTV 55
DB 262 LPMFTDYCVSDPESTAPKNGYVTGLPERKHLNDGVDVYLCCPMPVNAVRTHLSDG 321
QY 56 -----PSKPGTASPCWPLGAVPSPTVSRLEALTRAQ 88
DB 322 SVTNFYFEKFNNSATPGAAP-----APRPERELEATRAAE 359

RESULT 13
Q9PB03
ID Q9PB03 PRELIMINARY; PRT; 554 AA.
AC Q9PB03;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Beta (1-3) glucanoyltransferase Gel3p (Fragment).
GN Name=GEL3;
OS Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5085;
RX [1]
SEQUENCE FROM N.A.
RP STRAIN=CBS 144. 89;
RX MEDLINE=20233679; PubMed=10769178;
RA Mouyna I., Monod M., Fontaine T., Henriess B., Lechevalier B.,
RA Latge J.P.;
RT "Identification of the catalytic residues of the first family of
RT beta(1-3)glucanoyltransferases identified in fungi."
RL Biochem. J. 347:741-747(2000).
DR EMBL: AF208040; AAF40140.1; -.
DR GO: GO:0016740; F:transferase activity; IEA.
DR InterPro: IPR004886; GAST.
DR Pfam: PF03198; GAST; 1.
KM NON TER 554
SQ SEQUENCE 554 AA; 58097 MW; 57D0236A74D44ADA CRC64;

Query Match 12.9%; Score 77; DB 2; Length 554;
Best Local Similarity 25.0%; Pred. No. 94;
Matches 34; Conservative 17; Mismatches 51; Indels 34; Gaps 6;

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QY 7 LLLPFLTKSVFCSLVTSYLPTNTEDLSL-----WLMKPD-----LHSGRTVSTHV 53
DB 281 VLFPGMDVWVSGGIYMYFETINDYGLVSVGSANVTPEDFYLSSEIOSATPTGVNSH 340
QY 54 TV-----PSKPGTASPCWPLAGAVPSP-----TVSRLEALTRAVQVAPPLGSG-- 95
DB 341 SPSPTNSPACPCPTVDPTW-LAKSGPLPPIPMALGSCWVSSLSGVKDSVDMEKYGELFG 399
QY 96 --CGFGGCGPCPRRRD 109
DB 400 QVCGYGGGICDGIARN 415

RESULT 14
Q8XSC3 PRELIMINARY; PRT; 401 AA.
ID Q8XSC3;
AC Q8XSC3;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE PROBABLE CHROMATE TRANSPORT TRANSMEMBRANE PROTEIN.
GN Name=chrA; Synonyms=RS03924; OrderedLocustNames=RS0555;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxId=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Gentin S., Artiguenave F., Gouy J., Mangenot S.,
RA Ariat M., Billault A., Broctier P., Camus J.C., Catolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weisenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646079; CAD17706.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0015109; F:Chromate transporter activity; IEA.
DR GO; GO:0015703; P:Chromate transport; IEA.
DR InterPro; IPR003370; Chromate_transp.
DR Pfam; PF02417; Chromate_transp. 2.
DR TIGRPFAMs; TIGR00937; 2A51; 1.
KW Complete proteome; Plasmid; Transmembrane.
SQ SEQUENCE 401 AA; 42639 MW; E6B5C13BBD66CB6C CRC64;

Query Match 12.9%; Score 76.5; DB 2; Length 401;
Best Local Similarity 34.3%; Pred. No. 74;
Matches 24; Conservative 8; Mismatches 33; Indels 5; Gaps 3;

QY 2 LWWLVLLPFLTKSVFCSLVTSYLPTNTEDLSLWMPKPD--LHSGRTVSTHVPSKP 59
DB 159 LMLVLTVALTATVTVSEVAVMLFLAG--GVLVLMRAPPKMLRQGLNAVAAAPTPAAS 216
QY 60 GTASPC-WPL 68
DB 217 GILGTIDWPL 226

RESULT 15
Q8NCU7 PRELIMINARY; PRT; 369 AA.
ID Q8NCU7;
AC Q8NCU7;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Guo J.H., Yu L.;
RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF506446; AAM28197.1; -.
DR InterPro; IPR008973; C2_Calb.
KW Hypothetical protein.
SQ SEQUENCE 369 AA; 39755 MW; 469963F6069A3CF1 CRC64;

Query Match 12.8%; Score 76; DB 2; Length 369;
Best Local Similarity 29.2%; Pred. No. 76;
Matches 31; Conservative 13; Mismatches 50; Indels 12; Gaps 3;

QY 8 LLLPFLTKSV-----FCSLVTSYLPTNTEDLSLW--LMPKPDLS-----GRTVSTHV 55
DB 91 LSLPHLPVRVTRVYGCALLSPHTRKESLLLGPPAPRAHYTGCGGCPDALLGTLRV 150
QY 56 PSKPGTASPCWPLAGAVSPPTVSRLEALTRAVQVAPPLGSGCGFGG 101
DB 151 PPAFGPATPAACCPRPQDALARPRGCRLLRVDPGLSRALRAG 196

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Search completed: December 25, 2004, 16:33:17
 Job time : 96 secs

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; NUMBER OF SEQ ID NOS: 33142

LENGTH: 654
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18441

Query Match 13.7%; Score 81.5; DB 4; Length 654;
Best Local Similarity 26.4%; Pred. No. 1.6;
Matches 33; Conservative 8; Mismatches 41; Indels 43; Gaps 6;

QY 27 PNTEDLSLM-----LMPKPDHSGRT-----EVSHTHP-SKPGTASPC----- 65
DB 4 PPTRSNHPACTASTATPSPPTSSSIRAPRPGPAATSPITKATPASPSPCASPS 63
QY 66 ---WPLAGAVSPPTVS--LEALTTRAVQVAEP-----LSCCGFGGPGC 103
DB 64 SPTWKTSAPSPPTANGWMTSAMTAARCSAHNENGRKGRSSRRSGAAGFSGFAA 123
QY 104 PGRRR 108
DB 124 PSRRR 128

RESULT 3
US-09-252-991A-25639
Sequence 25639, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25639
LENGTH: 134
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25639

Query Match 12.6%; Score 75; DB 4; Length 134;
Best Local Similarity 27.2%; Pred. No. 1;
Matches 34; Conservative 10; Mismatches 43; Indels 38; Gaps 7;

QY 2 LMTVLTLTLTKSVFCSLVTSYLPNTEDLSLMLWPKPDHSGTRTEVST--HTVPSK 58
DB 26 VWM-----KPTVSTAMTS--TSSRAPST-----WPTT--SGCCRRPSSMCASITPPGR 68
QY 59 PGTAFCMPPLAGAV-----PSPVTSRLLEALTTRAVQVAEPGSGCGFGGPGC 103
DB 69 ASISSSSWMPSPFICTTACTCLICRPWAKSTISSRSSTTRA--ATACGSRRTARA 125
QY 104 PGRRR 108
DB 126 PSRRR 130

RESULT 4
US-08-581-148C-16
Sequence 16, Application US/08581148C
Patent No. 6060644
GENERAL INFORMATION:
APPLICANT: Schnable, Patrick S.
APPLICANT: Robertson, Donald S.
APPLICANT: Hansen, Joel D.
APPLICANT: Nikolaou, Basil J.
APPLICANT: Xu, Xiaojie
APPLICANT: Xia, Yijie
TITLE OF INVENTION: ISOLATION AND USE OF CUTICULAR LIPID

TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,148C
FILING DATE: 29-DEC-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Larcher, Carol
REGISTRATION NUMBER: 35243
REFERENCE/DOCKET NUMBER: 71380
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 555 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-581-148C-16

Query Match 12.5%; Score 74.5; DB 3; Length 555;
Best Local Similarity 30.9%; Pred. No. 7.5;
Matches 30; Conservative 10; Mismatches 44; Indels 13; Gaps 6;

QY 3 W-LT-VL-LTLPTLTKSVFCSLVTSYLPNTEDLSLMLWPKPDHSGTRTEVSTHTVPSKPGT 61
DB 25 MWDNMNVIMQTL--IAAVLTSRVPATSDLSAM-----DLR-GMALVAVLVAAVSEPAF 76
QY 62 ASFCMPPLAGAVSPPTVSRLLEALTTRAVQVAEPGSGCGF 98
DB 77 ---YMAHRAHLHLGFLPSRYHLSHSFOATQAL-TAGF 109

RESULT 5
US-09-489-039A-14266
Sequence 14266, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 14266
LENGTH: 124
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14266

Query Match 12.4%; Score 73.5; DB 4; Length 124;
Best Local Similarity 30.7%; Pred. No. 1.4;
Matches 23; Conservative 6; Mismatches 35; Indels 11; Gaps 3;

QY 38 PKPDHSGTRTEVSTHTVPSKPGTASPCMPPLAGAV-----PSPVTSRLLEALTTRAVQV 89
DB 15 PGPASRAGSEKASPPAFA-PGSAHPA--AAGAVGSSAPGRWPAARRRRSGSPAVFA 71

RESULT 12
US-09-252-991A-30613
; Sequence 30613, Application US/09252991A

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1      RESULT 13
2      US-08-095-734-2
3      Sequence 2, Application US/08095734
4      Patent No. 5807723
5      GENERAL INFORMATION:
6      APPLICANT: Aldovini, Anna
7      APPLICANT: Young, Richard A.
8      TITLE OF INVENTION: Homologously Recombinant Slow Growing
9      TITLE OF INVENTION: Mycobacteria and Uses Therefor
10     NUMBER OF SEQUENCES: 2
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
13     STREET: Two Millitia Drive
14     CITY: Lexington
15     STATE: MA
16     COUNTRY: USA
17     ZIP: 02173
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: Floppy disk
20     COMPUTER: IBM PC compatible
21     OPERATING SYSTEM: PC-DOS/MS-DOS
22     SOFTWARE: Patentin Release #1.0, Version #1.25
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/08/095,734
25     FILING DATE: 22-JUL-1993
26     CLASSIFICATION: 435
27     ATTORNEY/AGENT INFORMATION:
28     NAME: Granahan, Patricia
29     REGISTRATION NUMBER: 32,227
30     REFERENCE/DOCKET NUMBER: WH193-11M
31     TELECOMMUNICATION INFORMATION:
32     TELEPHONE: 617-861-6240
33     TELEFAX: 617-861-9540
34     INFORMATION FOR SEQ ID NO: 2:
35     SEQUENCE CHARACTERISTICS:
36     LENGTH: 1271 amino acids
37     TYPE: amino acid
38     STRANDEDNESS: single
39     TOPOLOGY: linear
40     MOLECULE TYPE: protein
41     US-08-095-734-2

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Query Match 11.8%; Score 70; DB 1; Length 1271;
Best Local Similarity 23.7%; Pred. No. 70;
Matches 37; Conservative 10; Mismatches 59; Indels 50; Gaps 7;
QY 2 LWWL-----VLLLPPLKSVFCSLYTSLYLP-NTBLSLIMLPKPLHSG 45
DB 1060 IWWLARGLEFPDGEFGELLPFTNPTGAFQFLLYVVVDLPFHIAQIATWLGQYPLLGA 1119
QY 46 TRTEVSTH-----TVPSK--PGTASPCMPPLAGVPS-----74
DB 1120 ALTGVAHGLGATGLAGLSGLSAIPSAIPVAVPELTVPVAAAPMLAVAGVPAVAPGM 1179
QY 75 -PTVSRLEALTRAVQVABPL-GSCGFGGPGC-PGR 107
DB 1180 LPASAPAPAAAAGATAGTTPPTGFGGLPALPGR 1215

RESULT 14
US-08-444-623-2
Sequence 2, Application US/08444623
Patent No. 5866403
GENERAL INFORMATION:
APPLICANT: Aldovini, Anna
APPLICANT: Young, Richard A.
TITLE OF INVENTION: Homologously Recombinant Slow Growing
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,623
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/095,734
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: 07/711,334
FILING DATE: 06-JUN-1991
APPLICATION NUMBER: 07/367,894
FILING DATE: 19-JUN-1989
APPLICATION NUMBER: PCT/US90/03451
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: PCT/US89/02962
FILING DATE: 07-JUL-1989
APPLICATION NUMBER: 07/361,944
FILING DATE: 05-JUN-1989
APPLICATION NUMBER: 07/223,089
FILING DATE: 22-JULY-1988
APPLICATION NUMBER: 07/216,390
FILING DATE: 07-JUL-1988
APPLICATION NUMBER: 07/163,546
FILING DATE: 03-MAR-1988
APPLICATION NUMBER: PCT/US88/00614
FILING DATE: 29-FEB-1988
APPLICATION NUMBER: 07/020,451
FILING DATE: 02-MAR-1987
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI93-11M2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-444-623-2

Query Match 11.8%; Score 70; DB 2; Length 1271;
Best Local Similarity 23.7%; Pred. No. 70;
Matches 37; Conservative 10; Mismatches 59; Indels 50; Gaps 7;
QY 2 LWWL-----VLLLPPLKSVFCSLYTSLYLP-NTBLSLIMLPKPLHSG 45
DB 1060 IWWLARGLEFPDGEFGELLPFTNPTGAFQFLLYVVVDLPFHIAQIATWLGQYPLLGA 1119
QY 46 TRTEVSTH-----TVPSK--PGTASPCMPPLAGVPS-----74
DB 1120 ALTGVAHGLGATGLAGLSGLSAIPSAIPVAVPELTVPVAAAPMLAVAGVPAVAPGM 1179
QY 75 -PTVSRLEALTRAVQVABPL-GSCGFGGPGC-PGR 107
DB 1180 LPASAPAPAAAAGATAGTTPPTGFGGLPALPGR 1215

RESULT 15
US-08-471-869-2
Sequence 2, Application US/08471869
Patent No. 6022745
GENERAL INFORMATION:
APPLICANT: Aldovini, Anna
APPLICANT: Young, Richard A.
TITLE OF INVENTION: Homologously Recombinant Slow Growing
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,869
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08267
FILING DATE: 22-JUL-1994
APPLICATION NUMBER: US 08/095,734
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 07/711,334
FILING DATE: 06-JUN-1991
APPLICATION NUMBER: 07/367,894
FILING DATE: 19-JUN-1989
APPLICATION NUMBER: PCT/US90/03451
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: PCT/US89/02962
FILING DATE: 07-JUL-1989
APPLICATION NUMBER: 07/361,944

1 FILING DATE: 05-JUN-1989
 2 PRIOR APPLICATION DATA:
 3 APPLICATION NUMBER: US 07/223,089
 4 FILING DATE: 22-JUL-1988
 5 PRIOR APPLICATION DATA:
 6 APPLICATION NUMBER: US 07/216,390
 7 FILING DATE: 07-JUL-1988
 8 PRIOR APPLICATION DATA:
 9 APPLICATION NUMBER: US 07/163,546
 10 FILING DATE: 03-MAR-1988
 11 PRIOR APPLICATION DATA:
 12 APPLICATION NUMBER: PCT/US88/00614
 13 FILING DATE: 29-FEB-1988
 14 PRIOR APPLICATION DATA:
 15 APPLICATION NUMBER: US 07/020,451
 16 FILING DATE: 02-MAR-1987
 17 ATTORNEY/AGENT INFORMATION:
 18 NAME: Granahan, Patricia
 19 REGISTRATION NUMBER: 32,227
 20 REFERENCE/DOCKET NUMBER: WH193-11MA2
 21 TELECOMMUNICATION INFORMATION:
 22 TELEPHONE: 617-861-6240
 23 TELEFAX: 617-861-9540
 24 INFORMATION FOR SEQ ID NO: 2:
 25 SEQUENCE CHARACTERISTICS:
 26 LENGTH: 1271 amino acids
 27 TYPE: amino acid
 28 STRANDEDNESS: single
 29 TOPOLOGY: linear
 30 MOLECULE TYPE: protein
 31 US-08-471-869-2

Query Match	11.8%	Score 70	DB 3	Length 1271
Best Local Similarity	23.7%	Pred. No. 70		
Matches 37, Conservative	10	Mismatches 59	Indels 50	Gaps 7

[illegible]

Search completed: December 25, 2004, 16:33:44
Job time : 24 secs